

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 18:11:29 ; Search time 4492.43 Seconds
(without alignments)
6503.779 Million cell updates/sec

Title: US-09-830-647-4

Perfect score: 2719

Sequence: 1 aatctgcgcgcgcgcctctctg.....aaaaaaaaaacctcgcag 2719

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthm:*
3: em_estln:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estoy:*
9: em_hc:*
10: gb_estl:*
11: gb_est2:*
12: gb_hc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887.6	32.6	950	10	AL560180
2	817	30.0	845	10	AL581669
3	769	28.3	769	10	AL548911
4	768.2	28.3	784	10	AL573294
5	753.4	27.7	1019	11	BG720949
6	723.4	26.6	725	10	AL559244
7	721.6	26.5	903	10	AL128881
8	719	26.4	742	10	AL580899
9	710	26.1	744	10	AI948485
10	696.4	25.6	821	11	BG462889
11	692.4	25.5	703	11	BG716928
12	691.6	25.4	767	11	BG717397

13	686	25.2	712	11	BF793466
14	671.4	24.7	701	10	AW960753
15	661.4	24.3	743	10	AT761101
16	647	23.8	730	10	AM105287
17	645.4	23.7	659	10	BE613476
18	639.4	23.5	927	11	BG025871
19	607	22.3	2338	12	AK014480
20	597.8	22.0	603	10	AT824033
21	593	21.8	616	11	BE884320
22	586	21.6	701	11	BG722508
23	585	21.5	585	11	BG724408
24	574.8	21.1	581	11	BG719249
25	572	21.0	670	10	AV645569
26	568.2	20.9	706	11	BI094492
27	562.8	20.7	950	11	BE88697
28	561.6	20.7	839	10	BE564084
29	561	20.6	561	10	AA451820
30	560.4	20.6	578	11	BG724066
31	553	20.3	639	10	AV728361
32	548.6	20.2	935	11	BG341292
33	548	20.2	549	10	AI923577
34	545.2	20.1	571	10	AU150504
35	540.2	19.9	760	11	BF219022
36	530.4	19.5	629	11	BE888268
37	523.8	19.3	839	10	BE782351
38	493.4	18.1	570	10	AU143969
39	490.4	18.0	493	10	AI452459
40	488.6	18.0	626	10	BE245831
41	484.2	17.8	489	10	AW967974
42	478.2	17.6	557	10	AW591976
43	474	17.4	474	10	AI452802
44	470	17.3	470	10	AI217171
45	468.2	17.2	484	10	AT797599

ALIGNMENTS

RESULT 1
AL560180 950 bp mRNA EST 16-FEB-2001
LOCUS AL560180 LTI_Fl011_BCl Homo sapiens cDNA clone CS0DG002YE20 5 prime
DEFINITION , mRNA sequence.
ACCESSION AL560180.1 GI:12906394
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Human.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DG002YE20"
/clone_lib="LTI_Fl011_BCl"
/sex="male"
/tissue="B cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen

9800 Medical Center Drive Rockville, Maryland 20850, USA
 Fax : (1) 301 610 8371 Email : filangellifotech.com URL :
 http://fulllength.invitrogen.com*

BASE COUNT 303 a 204 c 209 g 232 t 2 others
 ORIGIN

Query Match 32.6% Score 887.6; DB 10; Length 950;
 Best Local Similarity 99.9%; Pred. No. 4.5e-134;
 Matches 887; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

AL581669/c AL581669 845 bp mRNA EST 16-FEB-2001
 LOCUS AL581669 LTI_FL011_BCI Homo sapiens CDNA clone CS006002YE20 3 prime
 DEFINITION ' mRNA sequence.
 ACCESSION AL581669
 VERSION AL581669.1 GI:12948899
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 845)
 AUTHORS Li, W.-B., Gruber, C., Jessee, D., and Polayes, D.
 TITLE Full-length CDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 Source
 1.845
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS006002YE20"
 /clone_11p="LTI_FL011_BCI"
 /sex="male"
 /tissue_type="B cells from Burkitt lymphoma"
 /lab_host="DH10B"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filangellifotech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 216 a 146 c 154 g 307 t 22 others
 ORIGIN

Query Match 30.0% Score 817; DB 10; Length 845;
 Best Local Similarity 96.8%; Pred. No. 1.2e-122;
 Matches 818; Conservative 22; Mismatches 4; Indels 1; Gaps 1;

OY 2041 catgattctgctgatacaataaagcgttcacagaagccacttaactggttcaaggcaag 2100
 Db 425 CATGATTCGCGTGTGATTAACATTAACAGTTTCACAAGAGCACCCTAAGTGTTCAGGCAAG 366
 OY 2101 gctccatccatcaccctccctcgaaggaaacccaatgtaatgtgaacttaagaatgtgatagt 2160
 Db 365 GCCCATTCCTCMTCMCCCCCCTSMSSMCCCAATGATGTSACTTCAAGAAATATGTGATAGT 306
 OY 2161 ttaacctctggttaaatacatcgtgaaagtgaataataataataataataataataataataata 2220
 Db 305 TTMCBBTCTGTRAAATACATGCAAAAGKRRATTAATTAAGAGCAATATGAAAGAA 246
 OY 2221 aatctggaaccaaatgctgtaatttgataaagaagaactgaaatttattacacaaagaagaanc 2280
 Db 245 AATCTGGAACCAATGCTGAATTTGATTAAGACATGAACTTTATTACACAAAGAGAAAC 186
 OY 2281 agaatttgatgtacccggttacagtccttactagactgtgttcagaactgtaagaaga 2340
 Db 185 AGAAATTTGTTGTTACCCGTTACAGTCTTACTAGACTTGTTCAGACTGTAGTGAAGAA 126
 OY 2341 tcaagatttttggtgttcaacaagctacacagaagaagagtgatataatgtcaatgttttaagt 2400
 Db 125 TCAGATTTTGGTGTTCACAGTACAGCAAGAGAGTGTATATGCAATGTATTAGAT 66
 OY 2401 atttggaagaagaataatcagataatctgttaacagcgttttctcgtcccttcaact 2460
 Db 65 ATTAGGAAGAGAAATTCAGATATCTGTTACACAGCGTTTCTCGTCCCHTCACT 6
 OY 2461 tctac 2465
 Db 5 TCTAC 1

RESULT 3
 AL548911 769 bp mRNA EST 16-FEB-2001
 LOCUS AL548911 LTI_NFL006.PL2 Homo sapiens cdna clone CS0D1043Y010 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL548911
 VERSION AL548911.1 GI:12884384
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 769)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
 FEATURES
 source
 1..769
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1043Y010"
 /clone_lib="LTI_NFL006.PL2"
 /issue_type="Placenta"
 /note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pcMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifestech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 249 a 168 c 170 g 182 t
 ORIGIN

Query Match 28.3%; Score 769; DB 10; Length 769;
 Best Local Similarity 100.0%; Pred. No. 6,9e-115;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 339 agccgagtcgccccccggaacccgacctcgcagacgcggttacctactcgttagagcc 398
 Db 1 AGCCGATCCGGCCCGGGAACCCGACCTGCAGACCGGGTACTCTACTCGGTAAGAGCC 60
 OY 399 gtagctggcggaagagagagcgccgctcctgtaacagcgccgggggaagccggtctt 458
 Db 61 GTAGCTGGGGGAAGGAGAGGGGGCGCTCTGTCAACAGCGCGGGGAAGCGGTCTTT 120
 OY 459 ccgctgcccgggtgcagacttctcggaccacagatgagtgccggcgagccca 518
 Db 121 CCGCGCTGCCCGGTCCGACACTTCTCCGGACCCACACTGTAGGTCCGGCGACTGCCA 180
 OY 519 tgaactccgagccatgagagatccacagtaagagacattccagggtggatccagta 578
 Db 181 TGAACTCCGGAGCCATGAGGATCCAGTAAGAGACATTTCCAGGGTGGAAATCAAGTCA 240
 OY 579 aaaaagaaaaaacagacacatctcgaatctcgaacacgtacacagccagaaaaat 638
 Db 241 AAAATGAAAAAACAAGACCATCTCTGAAATCTCTGAAACTGATAACAGGCCAGAAAAAT 300
 OY 639 ccaaatgtagccactttggggaagaagtatttacttgacttaactctctgtacatat 698
 Db 301 CCAAAATGTAAAGCCACTTGGGGAAGATATTTTACCTTCACTTCTGTACCATAT 360
 OY 699 ctgaanaacttcaaaagacatlaagatctggagggcaggttgagaatttcagca 758
 Db 361 CTGAAAAACTTCAAAAGGACATTAAGATCTGGAGGGGAGTGAAGAAATTTCTAGCA 420
 OY 759 aagatatacgtatcttatttcaataaagaagaagctaaatttgacaaaccttggatc 818
 Db 421 AAGATATCAGTTATCTTATTTCATAAATGAAGAGACATTAATTTGCAACAACTTGAGTC 480
 OY 819 gaatttctctgtcacaagtcgaatctgcatactcgcagagaacacacttaccctatc 878
 Db 481 GAATTTCTCTGTATCCCAAGTCCAGAAATCTGCATATCTCGAGAAACACTTCACTCATC 540
 OY 879 ccagccatgatggaagttaatttaagtaacccagacagtggttttaagcagaagaaat 938
 Db 541 CCAAGCATGATGGAATTTCTTTAATGTCACACACAGTGTGTTTAAGCAGAGGAAAT 600
 OY 939 tattaagtgaanaagctatcaagaagacatgatttatttccctcaaatagatataatca 998
 Db 601 TATTAGTTGAAAAAGCTATCAAGAGACCATGATTTATTCCTTCAAAATGATATATCA 660
 OY 999 atgcttgcacagggagtaaaaaatctctcatatgtagacatagatataatgaac 1058
 Db 661 ATGCCCTTGATCGGGGAGTAAAAATCTTCATTTATGATGACATTAATCAATTGAAC 720
 OY 1059 aaaaagaaaaagagtgtagtatttactcaagaataatcaagtaactgaagaag 1107
 Db 721 AAAAGAAAAAGAGTTGTATTATCTCAAGAAATCAAGTACTTGATGAAG 769
 RESULT 4
 AL573294 784 bp mRNA EST 16-FEB-2001
 LOCUS AL573294 LTI_NFL006.PL2 Homo sapiens cdna clone CS0D1043Y010 3
 DEFINITION prime, mRNA sequence.
 ACCESSION AL573294
 VERSION AL573294.1 GI:12932397
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 784)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization

QY 457 ttccgagctgcccggtgacacattctccgagaccacgaatgagtcgaggagactgc 516
 |||
 Db 125 TTCCGGGCTGCCCGGTGGACACTTCTCCGGACCCAGCATGTAGTGGCGGCACCTGC 184
 QY 517 catgaactccgagacatgagatcacagtaaaagacattccagggtgagatccaagt 576
 |||
 Db 185 CATGAACCTCCGAGCATGAGGATCCACAGTAAGACATTGCCA-GGTGGAATCCAACT 243
 QY 577 caaaaatgaaaaaagacacacatctctgaaatctctgaaaactgataaaggccagaaa 636
 |||
 Db 244 CAAAATGAAAAAACAACACATCTCTGAAATCTGAAAACGTATACAGGCCAGAAAA 303
 QY 637 atccaaatgtaagcactctggggaaaagatattactcttgactcctctgtacact 696
 |||
 Db 304 ATCCAAATGTAGGCACCTTGGGGAAAAAGTATTTTACCTTGACTTACCTTGTGCACCAT 363
 QY 697 atctgaaaactccaagaagacatgaagatctggagggcgagcttgaagaattctctag 756
 |||
 Db 364 ATCTCAAAAACCTTCAAAAAGACATTAAAGATCTGGGAGGCGCAAGTTGAAGAAATTTCTCAG 423
 QY 757 caaagatatacgtatctctattca-ataaagaagaagctaaattlgacacaaacttg 814
 |||
 Db 424 CAAAGATATTCAGTATCTTATTCAACATTAAGACGGAAGCTAAATTTGCCAACAACCTTG 483
 QY 815 ggtcgaatttctctgtacccaagtccagaatctgcatactgcgaagaacacacttcact 874
 |||
 Db 484 GGTCAAAATTTCTCCCTGTACCAAGTCCAGACATCTGCATATCTGCAAGAACCCACTTCACCT 543
 QY 875 catccacacatgataggaatgattcaatgaagacagacacagtggtgttaagcagaaga 934
 |||
 Db 544 CATCCACACCATGATGATGGAAGTTTCAATTAAGTACACAGACACAGTGTGTTAAAGCAGAGGA 603
 QY 935 aaatattatgataaagaacatacaaggacacataattatctcctcaaatagatata 994
 |||
 Db 604 AAATATTATGTTGAAAAAGCTATCAAGGACCATGATTTTATTCCTTCAAAATAGTATATTA 663
 QY 995 tcaatgctcgtctcgtgagggagtaaaatcttcaatctatgtagaa-ctagatctact 1053
 |||
 Db 664 TCAATATGCTTGTCTATGGGGAGTAAAAATCTTCAATTTGAGACACTTAATTAATTAATTA 723
 QY 1054 tgaacaaaagaagaagaagtttatttactcaagaatacaagtaac-ttcagtaagagatg 1112
 |||
 Db 724 TGACAAAAAGAAAAAGAGTGTATTTACTCAAGAAATCAAGTACTTTAGTAGAGCAATG 783
 QY 1113 ggggcaaaagattgtagtggtgagcaaaaaaacaagaacaggaagactcaaaaagcctt 1172
 |||
 Db 784 GGGGCAAAAAGAGTGTGTGTGGCAAAAACACAGCACCGGAGAACTCAGAGAGCCTT 843
 QY 1173 ttgta 1177
 |||
 Db 844 GGGTA 848
 RESULT 6
 LOCUS AL559244 725 bp mRNA EST 16-FEB-2001
 DEFINITION AL559244 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0D012YL06 5
 prime, mRNA sequence.
 ACCESSION AL559244
 VERSION AL559244.1 GI:12904555
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 725)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 Source
 1..725
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D012YL06"
 /clone_1lb="LTI_NFL008_TC2"
 /sex="male"
 /ruse_type="T" cells from T cell leukemia"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@life.com URL : <http://fulllength.invitrogen.com>"
 BASE COUNT 224 a 166 c 164 g 171 t
 ORIGIN
 Query Match 26.6%; Score 723.4; DB 10; Length 725;
 Best Local Similarity 99.9%; Pred.No. 1.6e-107;
 Matches 724; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 329 cgcgccttgagccgagatccgcccgcgaacccgacctgcagacgagctactactg 388
 |||
 Db 1 CGGGCTTGGAGCGGATATCGGGCCCGGAACCCGACGACGCGGACTTACTAGC 60
 QY 389 cgtagaagccgtatgctgaggaagaagagcgccgtctgtcaacagccgggggaa 448
 |||
 Db 61 CGTAGAGCGCGTAGCTGCGGGAGAGAGAGCGCGCGCTCTGTCAACAGCGCGGGGAA 120
 QY 449 gccgtccttgccgggtgcccgtgagacattctccgagaccagcatgtagtcgag 508
 |||
 Db 121 GCCGTCTTTCGGCGCTGCCCGGCGGACACTTCTCCGGACCCACATGTAGTCCCG 180
 QY 509 ggcactgcatgaactccgagccatgagatccacagtaaaagacattccagggtgaa 568
 |||
 Db 181 GGCACATATGTAAGCTCCGAGCATGAGGATCCACAGTAAGACATTTCCAGGGTGA 240
 QY 569 atccaaatcaaaaaaagacacacatctctgaaatctctgaaaactgataacagg 628
 |||
 Db 241 ATCCAAAGTCMAAAATGAAAAAACAACACATCTCTGAAACTGTATACAGG 300
 QY 629 ccagaaaatccaaatgtaagccacttgggaaaagatttacttgactactctt 688
 |||
 Db 301 CCAGAAAAATCCAAATGTAAAGCCACTTTGGGGAAAAAGTATTTACTTGAATTA 360
 QY 689 gtacacatactgaaaaaacttcaaaagacatgaagatctggagggcgagttgaaga 748
 |||
 Db 361 GTCCACCATATTCGAAAAACCTTCAAAAGGACATTAAGATCTGGAGGGAGTTGAAGAA 420
 QY 749 tttctcagaagaagatagttatcttatttcaataaagaagaactaaattgcaaa 808
 |||
 Db 421 TTTCTTAGGAAATATATGATTTATTTTCAAAAGAGGAAAGAACTAAATTTGCACAA 480
 QY 809 acctgggtcgaaattctctctgacccaagctccgaatctgcatactcagaagaacct 868
 |||
 Db 481 ACCTTGCGTCGAATTTCTCTGTACCAAGTCCGAAATCTACATATACTGAGAAACACAG 540
 QY 869 caactcatccagcagatgagatcaatttaagtcaccagacagtgltgtaagc 928
 |||
 Db 541 TCACCTCATCCAGCCCATATGAGAACTTAAATTAAGTCAACAGACAGTGTATTAAGC 600
 QY 929 agaggaataatttagtgaagaagatcaagagaccatgatttcttctaataagt 988
 |||
 Db 601 AGAGGAAATTAATTAATTAAGAAAGCTATCAAGGACCATGATTTTATCTTCAAAATAG 660
 QY 989 atattcaaatgctgtcatgaggagtaaaatcttcatattgatatgatatagac 1048
 |||

```

Db      661 AATATTCAAAATGCTTGTGTCATGGAGTAAATTTCTTCATTTGATGACATTGATATC 720
OY      1049 tacat 1053
        |||||
Db      721 TACAT 725

RESULT 7
LOCUS   AUI28881 903 bp mRNA EST 24-OCT-2000
DEFINITION AUI28881 NT2RP2 Homo sapiens cDNA clone NT2RP2004396 5', mRNA
sequence.
ACCESSION AUI28881
VERSION   AUI28881.1 GI:10989235
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 903)
Ota.T., Nishikawa,Y., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Ishigai,T.
HRI human cDNA project
Unpublished (2000)
JOURNAL Genomics Laboratory
COMMENT Helix Research Institute
153-3 Yana, Kishigazu, Chiba 292-0812, Japan
Tel.: 81-438-51981
Fax.: 81-438-52-3952
Email: genomics@helix.co.jp
HRI human cDNA project, 5'-, 3'-end one pass sequencing; Helix
Research Institute, cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
FEATURES
Source
1..903 nt/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2004396"
/clone_1lb="NT2RP2"
/clone_1lb="Hericarcinoma"
/est_1lb="NT2"
/vector="PMI8SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction;"
BASE COUNT 326 a 165 c 157 g 242 t 13 others
ORIGIN
Query Match 26.5% Score 721.6; DB 10; Length 903;
Best Local Similarity 92.3%; Pred. No. 3e-107;
Matches 820; Conservative 0; Mismatches 56; Indels 12; Gaps 6;

OY 1593 tatcttcgaagaagtcgcggaagaatgatacaagc-gaagaagcagaattcctgt 1651
Db 1 TATTTCTCAAAAAGTTCCAGGAAGATGATACACAGCGAAGAGCAGAAATTCTCTG 60
OY 1652 ataaagaagcccaagaagaactaaaaaagctcctgtttttttcagaagccatcccccacc 1711
Db 61 ATTAAGAGCCACGAGAAATCAAAAAAGCTCCTGTTTATTTTCACAGCCCATCCCCACC 120
OY 1712 ctccaataaattgagaggttaataagaagaatgtaataatggttcacatgttaagta 1771
Db 121 CTTCAAATGAATTGAGAGCGCTTAATGAGAAATGATTAATGTTCCATGTTAAGTA 180
OY 1772 cagctgaagaatacctaagaagaatttcacagctacactctacataaaacaacaag 1831
Db 181 CAGCTGAAGATGACNTAAGACAGAAATTTTACACAGCTACCTCTACATFAAAAAACAGG 240
OY 1832 atagcattcttaacatttcgacacacacttaagtaagtaaaactaagtaagaactaagg 1891
Db 241 AATGCATCTTGACATTCGCGAACACACATTAAAGTGAATAATGACTTAAGAGACTANGCG 300

```

```

OY 1892 tagatcactataatgatatacatagagcagctgtacatgtttctgatttcagtagacagata 1951
Db 301 TAGATCAGTATTAATGTAAATGTAACATACAGGCATCTGTACATGTTTCTGATTTCAAGTACA 360
OY 1952 atagtgatctcaaccacaaacagaagtcagatactgtgtttttccacaagaagatctca 2011
Db 361 ATAGTGATCTCACCAAAACAGAAAGTCAGATACGTGCTTTTCCACAAAGCATCTCA 420
OY 2012 aggaagaagaccttcattcaatatttactcatgattctgtgtctgtgataacaataagct 2071
Db 421 AGGAAAAGGACCTTCTTCAATATTTACTCATGATTCTGTCTGATTAACAATTAACAGTT 480
OY 2072 cacaagaagcacttaactgttcaggcaaaagctccatccatcactcctcctgaagagccca 2131
Db 481 CACAAAGCACCTAACTGTCAGCAGNAAGCTCCATTCATCTCCTCGAGGACCCCA 540
OY 2132 atgaatgtgactcaagaataatgtagtttactcctgtgtaaatatatacagaaagtga 2191
Db 541 ATGAATGTGACTTCAAGAAATATGATAGTTTACCCTCTGTGTAATAATACATCGAANAAGTGA 600
OY 2192 aaataatatta-ggaagaataagaagaataatctggaacccaatgctgaatttgataaa 2250
Db 601 AATTAATATTAGGAGCAAAATGAAAAGAAAATCTGGAACCAAAATGCTGAATTTGATTA 660
OY 2251 agaactgaatttatacacaaagaagaagaagaatgtgtagttcaacgggtacagctctta 2310
Db 661 AGAAGCTGAATTTATTTNCCCCAGACAAACNGAATTTGT-TTTCACCGGTACAGCTTTTA 719
OY 2311 ctgactgtttcagaagctagtgaaagaatacagaatlttggtgtttcacaagctacaca 2370
Db 720 CTANAAGCTTTCAAGTACAGTACGTAAGGAAAAAATCNAATTTTGGCTTCCAAAGCTACCCA 779
OY 2371 gaaa--gagtgatataatgaatgttttagaatttgg---aagagaataatcaga 2423
Db 780 GAAAAAAGAAATTGATATATCCATGTTTAAATATATGATGGGGAAGAAAAGAAAATTCNNAT 839
OY 2424 taactgttaacagcgtttt--ctcgccctcctcaactctacatt 2469
Db 840 AATCGGTAAACAGCGTTTTCGCCNGTCCTTCAACTTCCTCCWTT 887

RESULT 8
LOCUS   AL580899/c 742 bp mRNA EST 16-FEB-2001
DEFINITION AL580899 LRI_NFL008_Tc2 Homo sapiens cDNA clone CS0DV012YL06 3
prime, mRNA sequence.
ACCESSION AL580899
VERSION   AL580899.1 GI:12947367
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 742)
Ll.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Source
1..742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DV012YL06"
/clone_1lb="LRI_NFL008_Tc2"
/sex="male"
/tissue="T cells from T cell leukemia"
/note="Vector: PCMVSPORT 6; Site: 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime
enriched, double-stranded cDNA was digested with Not I and

```

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT 228 a 124 c 120 g 269 t 1 others
ORIGIN

Query Match 26.4%; Score 719; DB 10; Length 742;
Best Local Similarity 99.1%; Pred. No. 8.3e-107;

Matches 734; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

```

QY 1912 atcagcattcgtacatgcttctgattcagttacagataatagtgatctcacaacaa 1971
    |||||||
DB 742 ATACAGCATCTGTACATGTTCTGATTTCTAGTACAGATTAATAGTGTCAACCAAA 683

QY 1972 cagaagtcagatctgcttcttcagcaagatctcaaggaagaaagaccttattca 2031
    |||||||
DB 682 CAGAAGTCAGATCTGTCCTTTTTCACCAAGATCTCAAGGAAGACCTTCAATCA 623

QY 2032 atatttactcattcctgctcgtatcaacaaatcagttcacaagacactaactgt 2091
    |||||||
DB 632 ATATTACTCATGATCTGCTGCTGATTAACATTAACATTCACAGACACCTTAAGT 563

QY 2092 caggcaaaagctccatctcactcctcctcaggaagcccaatgaatgacttcaaga 2151
    |||||||
DB 562 CAGGCAAAAGCTCCATCTCATCTCTCTGAGAAACCAATGATGTACTTCAAGAA 503

QY 2152 atgataatttaccctctcgtgtaaaatatacagaagaatgaaatattatgagagaat 2211
    |||||||
DB 502 ATGGATATCTTACCTCTGCTGTAATATACATCAAGAAAGTGAATATATATAGACGA 443

QY 2212 agaaaagaagaatctcgaacccaatctgtaatttgaataaagactgaatttatacaca 2271
    |||||||
DB 442 AGAAAAGAAAATCTGGAACCAAAATGCTGATTTGATTAAGAAGATGATTTTACACA 383

QY 2272 gaagaaaacagaatttctgattcaccggtacagctcttactagactgcttcaagact 2331
    |||||||
DB 382 GAAGAAAACAGAAATTTGTAGTTCACCGGTACAGTCTTACTGACTGTTTTCAGACTAG 323

QY 2332 gaagagaatacagaatttctggtttcacaagctcacagaagaagaagtatagcaat 2391
    |||||||
DB 322 GAAGAGAATACAGAAATTTTGGTTTCAACAGCTACAGAAAGAGTGTATATGCAAT 263

QY 2392 gttttagatatttgggaagaggaataatcag--ataatcgttacaacgctttctcgt 2449
    |||||||
DB 262 GTTTAGATATTTGGGAAGAGGAATAATCAGCATACATCTGTTAACAGGTTTCTCTGT 203

QY 2450 ccccttcaactctacattacttgctttagaatttaaaaaatgacatttccaagaag 2509
    |||||||
DB 202 CCCCTTCAACTCTCTACATGTGACTGGCTTTTGAATCTAAAAATCATCTTTTCAAGAG 143

QY 2510 tgataagaataatcttctgaatttttaataatgtaatggaatctttagattttt 2569
    |||||||
DB 142 TGATAGAGATCATATTTCTGGAATTTTATTAATATGATGGAATTTCTAGATTTT 83

QY 2570 taccagcttcttacaacccaatgtaataataataataatctgcaatttcta 2629
    |||||||
DB 82 TACACGCTTTGTTTACACCAACCAATGTAATATTAATAATTAATTTGCAATTTTCTA 23

QY 2630 cagaatggaatacctgttaaa 2650
    |||||||
DB 22 CAGAAATGAAATACCTGTAA 2

RESULT 9
LOCUS A1948485 744 bp mRNA EST 08-MAR-2000
DEFINITION w96d08.x1 NCI-CGAP K1d12 Homo sapiens cDNA clone IMAGE:2470479 3'
Similar to TR:075226 075226 WUGSC:H_RG135C18.1 PROTEIN ; mRNA

```

```

sequence.
ACCESSION A1948485
VERSION A1948485.1 GI:5740795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/db/ftp/image/image.html
Insert length: 1484 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 432.
FEATURES
    source
        1..744
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:2470479"
        /clone_1db="NCI-CGAP K1d12"
        /tissue_type="2 pooled tumors (clear cell type)"
        /lab_host="DH10B"
        /note="Organ: kidney; Vector: pT73D-Pac (pharmacia) with
        a modified polylinker; Site_1: Not I; Site_2: Eco RI;
        Plasmid DNA from the normalized library NCI-CGAP K1d5 was
        prepared, and as circles were made in vitro. Following HAP
        purification, this DNA was used as tracer in a subtractive
        hybridization reaction. The driver was PCR-amplified cDNAs
        from a pool of 5,000 clones made from the same library
        (clones 1323912-1325831, 1471368-1472903 and
        1492104-1493255). Subtraction by Bento Soares and M.
        Fatima Bonaldo."
BASE COUNT 223 a 127 c 117 g 277 t
ORIGIN
Query Match 26.1%; Score 710; DB 10; Length 744;
Best Local Similarity 97.3%; Pred. No. 2.4e-105;
Matches 722; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1900 tataatgtaacatacagcagcattctacatgcttctgattcagttacagataatagtgga 1959
    |||||||
DB 744 TATCAATGTAAACAAACAGCGCGTGTACATGTTTCTGATCTCAGTACATCATAGTGA 685

QY 1960 tctcaaccaaacagaagtcagatactgcttcttcagcaaggaatctcaaggaag 2019
    |||||||
DB 684 TCTCAACCAACAGAGAGTCAGATATCTGCTTTTCCAGCAAGATCTCAAGGAACAG 625

QY 2020 gaccttcatcaatttctcgaatgcttctgctcgtatcaataaagaagttcacaagaag 2079
    |||||||
DB 624 GACCTTCATTCGATATTTCTCATGTGTTCTGGTCTGATTAACATTAACAGTTTCAACAGAG 565

QY 2080 caactaacgttcaaggcaaggctccattccalactcctcctgaggaacccaatgaatgt 2139
    |||||||
DB 564 CACCTAACGTGTTCAAGCAAGGCTCCATTCATTCATCTCTGAGAGAACCAATGAATGT 505

QY 2140 gacttcaagaataatgatagttactcctctggttaaaatacatcatcgaagaatgaaataata 2199
    |||||||
DB 504 GACTTCMAAGAAATATGATAGTTTACTCTGTGTAATAATCATTCGAAAGTGAATAAATA 445

QY 2200 ttagaacgaataatagaataaataatctcgtaacaaatgctcgaaatttgataaagaactgaa 2259

```

```

|||||
Db 444 TTAGAGAAATGAAAGAAATCTGGACCAATGCTGAATTTGATTAAGAACTGAA 385
|||||
Oy 2260 ttctacacaagaagaacagaattctgtagtcaccggtacagcttactagactg 2319
|||||
Db 384 TTATATTACACAGAGAGAAACAGAAATTTGTAGTTCACCGGACAGCTTACTAGACTTG 325
|||||
Oy 2320 ttccagactagtagaagaagaatcagaattttgggtttccacagctacacagaagaagat 2379
|||||
Db 324 TTTCAGACTACTCAGAGAAATCAGAAATTTTGGGTTTCACAGCTACAGAGAAAGAT 265
|||||
Oy 2380 ggtatagcaatgttttagatatttgggaagaagaataatcagaatctgttaacagc 2439
|||||
Db 264 GGTATATGCAATGTTTATAGATTTGGAGAGAGAAATTCAGTATATCTGTTACAGCG 205
|||||
Oy 2440 ttcttcgtccctcacaactctacattactggtctttagaatttaaaatgcatc 2439
|||||
Db 204 TTTTCTGTCGCCCTTCACTCTCACTTACTGCTGCTTTAGAAATTTAAATGATAC 145
|||||
Oy 2500 ttccagaagtgaagaagacatctctgaatcttataaatalgtatggaattctt 2559
|||||
Db 144 TTTTCAGAGTGAATGAAGATCAATATCTTGAAATTTTATTAATATGTAAGAAATCTT 85
|||||
Oy 2560 aggatcttttaccagctgtgtttacagaccacaatgttaaatlaaataaatattg 2619
|||||
Db 84 AGATATTTTACAGCTGTTGTTACAGACCAATGTAATATTAATAATTAATTTTG 25
|||||
Oy 2620 caattctcagaagattgata 2641
|||||
Db 24 AAAATTTCTAAAAAATAAAAAA 3
|||||

RESULT 10
Bg496289 821 bp mRNA EST 27-MAR-2001
LOCUS 602538259F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:465946 5',
DEFINITION mRNA sequence.
ACCESSION Bg496289
VERSION Bg496289.1 GI:13457805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 821)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strassberg, Ph.D.
Email: rgs@rs-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Invitae Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16M435 row: e column: 15
High quality sequence stop: 742.
Location/Qualifiers
1. 821
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:465946"
/clone_lib="NIH_MGC_59"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (TI phase-resistant)"
/notes="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgagc); Site_2: SfiI (ggcgctcgagc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTTGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCAGCGCCGACATG-dT(30)BN-3'

```

```

BASE COUNT 273 a 166 c 176 g 206 t
ORIGIN
Query Match 25.6%; Score 696.4; DB 11; Length 821;
Best Local Similarity 97.2%; Pred. No. 3,7e-103;
Matches 762; Conservative 0; Mismatches 16; Indels 6; Gaps 5;
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 clones
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."

Oy 417 gaagcgagccgtctctgcaacagcgagggaagccgtgcttgcggctgcgcgggtgga 476
|||||
Db 1 GAGCGGCGCTCTGTCACACAGCGCGGGAAGCCGTGCTTGGCGCGCTGCCGGTGGCA 60
|||||
Oy 477 caatttcgccgagccagcagatgtaggtgcggcgactgccatgaaatccggagccatga 536
|||||
Db 61 CACTTGTCCGACCCAGCATGTAGTGTCCGGGCACTGCCATGAATCTCCGAGCATGA 120
|||||
Oy 537 ggaatccagtaagaagacattccaggttggaatccaaatgaaatgaaatgaaatgaaatg 596
|||||
Db 121 GGATCCACAGTAAGGACATTTCCAGGCTGGAATCCAAATGCAAAAAACAGAC 180
|||||
Oy 597 catctcgaatctctgaaactga taacagggccagaaatccaaatgtaagccactt 656
|||||
Db 181 CATCTCGAATCTGTGAATACTGATAACAGGCCAGAAATCAATGTGAATGACCATTT 240
|||||
Oy 657 ggggaagaatatttacccttgaacttacccttctgacacatattgaaatgaaatgaaatg 716
|||||
Db 241 GGGGAAAGATTTTACCTTGACTTACTTCTGTGACATATGTGAAATCTTCAAAAG 300
|||||
Oy 717 acattaagatctcggagggcgagttgaagaatttcacagaagatcagttacta 776
|||||
Db 301 ACATTAAAGATCTGGAGGCGAGTGAAGATTTCTACACAAAGATACATTTATCTTA 360
|||||
Oy 777 ttcaaaataagaagaagctaaatttcacaaaccttgaggctgaattctcctgtaccaa 836
|||||
Db 361 TTTCAATTAAGAAAGGAAGCTTAATTTGCACAAACCTTGGGTGCAATTTCTCTGTACAA 420
|||||
Oy 837 gtccagaatctgatactatgcagaacaccttaccctcatccagcagatgtagaagt 896
|||||
Db 421 GTCCAGATCTGCATATCTGCGAGAAACCACTTCACTTCCACGCAATGATGGAAGTT 480
|||||
Oy 897 catttaagtcacagacacagtggttttaagcagaaggaatattatagttgaaatgaaatg 956
|||||
Db 481 CATTTAAGTCACAGACACAGTGTGTAAAGCAGAGAAATTAATTAAGTTGAAAAAGCTA 540
|||||
Oy 957 tcaagagcactgatttattctctcaaatagatattcaaatgctc-tgtcatgaggga 1015
|||||
Db 541 TCAAGAGCATGATTTTATTTCTCTCAATATGATATATCAAAATGCTTGTGATGGGGA 600
|||||
Oy 1016 gtaaaatcttataatgata-cattaagatctacatgtaacaaagaaagaaagagatt 1074
|||||
Db 601 GTAAAAATTTCTATATTTGATGACCTTATGACTACATTGAAAC-AAAGAAAGAAAGATG 659
|||||
Oy 1075 gtaattcctcaagaatcaagtaacttgcagtaagatgagtggaagaaggttgagagtg 1134
|||||
Db 660 GTATTATCTCAAAATCAAGTACTTCAAGTAAAGATGGGGCAAA--GAGTGTGATAGG 717
|||||
Oy 1135 tgcacaaaaaacaagaacagagacatcaaaagcctttgtaaaggtggaagatagag 1194
|||||
Db 718 TGCACAAAAAAACAAGAACAGAGAGATCAAAAGCCCTTTGT-AAAGTGCAATATAG 776
|||||
Oy 1195 ccaa 1198
|||||
Db 777 CCAA 780
|||||

RESULT 11
Bg16928

```


QY 1798 ttacacagctactcctctacataaaacacaggaatctctctgacatttcgcgaacac 1857
 DB 627 TTTACAGAGCTACCTCTACATTAATAAACAAGAGATGATCTTGGACATTTCCGACAC 686
 QY 1858 acattaagtgaatgacttagaaga 1883
 DB 687 ACATTAAGTGAATAAGACTTAGAGAGA 712

RESULT 14
 AM960753 701 bp mRNA EST 01-JUN-2000
 LOCUS AM960753
 DEFINITION EST372824 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM960753
 VERSION AM960753.1 GI:8150437
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gasparé,R., Gay,C., Holt
 ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johngetigf.org
 Plate: 150
 Seq primer: Reverse.
 FEATURES
 source Location/Qualifiers
 1..701
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGF"
 /note="Vector: pBluescriptSkm"
 BASE COUNT 240 a 140 c 147 g 173 t 1 others
 ORIGIN

Query Match 24.7%; Score 671.4; DB 10; Length 701;
 Best Local Similarity 98.8%; Pred. No. 4.1e-99;
 Matches 686; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 429 ctgtcaacagcgagggaagcgcgtgcttcgcgagtcgcgcgagtcgcgaacttcgcg 488
 DB 1 CTTGTAAACGCGCGGGGAGAGCCGTCCTTCCGCGCTGCCCGTGCGACACTTCTCCGG 60
 QY 489 acccgcatgtatgtgcccggcgagctgcataaactcgaagccatgaagatccacagta 548
 DB 61 ACCCGCATGTATGTGCGCGGCGAGCTGCCATTAATCCGAGCCATGAGATCCACAGTA 120
 QY 549 aaggaacttcacaggttggaaatccaaatgaaataaaacagacatctctgaaat 608
 DB 121 AAGGACATTTCCAGGCGTGAATCAAAATGMAAAAGAAAAACAGACATCTCTGAAT 180
 QY 609 ctctgaaaaactataacagggcagaataatccaaatgttaagccacttgggaaaaat 668
 DB 181 CTTCTGAAAACTATTAACAGCCAGAAAAATCCAAAGTAAAGCCACTTTCGGGAAAAAGTAT 240
 QY 669 ttacacttactactctctgtcacacatactgaaataaactcaaaaggacatlaagatc 728
 DB 241 TTTACTTACTTACTCTTGTGTACCATATCTGMAAACTTCAAAAGGACATTAAGATC 300
 QY 729 ttggagggcgagattgaagaattctcgaagaagatactcagttatctatcttaataaga 788
 DB 301 TGGAGGGCGAGATTGAAGAATTTCTCAGCAAGATATCAGTATCTTATTTCAATAAGA 360

QY 789 aggaagctaaatttcacaaacttgggtcgatcttctctgtaccgaatccagaatctg 848
 DB 361 AGGAAGCTAAATTTGGACAAACCTTGCGTGAATTTCTCTGTACCAATCCAGATCTG 420
 QY 849 catatactgcagaacacacttcacctcatccagcagcagatgagattcaatgaatc 908
 DB 421 CATATACCTGCAAAACCACTTCACCTCATCCAGCCATGATGAGATTCATTAAGTCAC 480
 QY 909 cagacacagtggtttaagcagaagaataattatgattgaaaaagctacagagaccatg 968
 DB 481 CAGACACAGTGTGTTAAACGAGAAATTTATAGTTAAAAAGCTATCAAGACCATG 540
 QY 969 atttattccctcaataatgatatcatcaaatgacctgtcat-999gagtaaaatctt 1027
 DB 541 ATTNTATTCCTTCAAAATATATATTTATCAAAATGCCCTTGTCATGGGGATTAATAATCTT 600
 QY 1028 catattgatacattagatactacattgaaacaaagaagaagattgattactcaag 1087
 DB 601 CATATGATGACATTTAGATTAATCAATTGAACAAAGAAAGAGTATTTACTCAAG 660
 QY 1088 aatcagatcttcgtaagatagatgggcaaaa 1121
 DB 661 AATCAAGTACTTTATATAGATGGGGCCCAA 694

RESULT 15
 A1761101/c 743 bp mRNA EST 21-DEC-1999
 LOCUS A1761101/c
 DEFINITION w169g03.x1 NCI-CGAP Kid12 Homo sapiens cDNA clone IMAGE:2398612 3'
 similar to TR:075226 075226 WUGSC:H_RG135C18.1 PROTEIN ;, mRNA
 sequence.
 ACCESSION A1761101
 VERSION A1761101.1 GI:5176768
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 743)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert length: 1678 Std Error: 0.00
 Seq primer: -40bp from Gibco
 High quality sequence stop: 437.
 FEATURES
 source Location/Qualifiers
 1..743
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2398612"
 /clone_lib="NCI-CGAP_Kid12"
 /clone_type="2 pooled tumors (clear cell type)"
 /tissue_type="Kidney"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pUT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 plasmid DNA from the normalized library NCI-CGAP_Kid5 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clones 1323912-1325831, 1471368-1472903 and
 1492104-1493255). Subtraction by Bento Soares and M.

Fri Dec 28 08:22:48 2001

us-09-830-647-4.rst

Page 12

BASE COUNT	227 a	124 c	115 g	277 t
ORIGIN	Fatima Ronaldo. "			

Query Match	24.38;	Score 661.4;	DB 10;	Length 743;
Best Local Similarity	97.28;	Pred. No. 1.7e-97;		
Matches 716; Conservative	0;	Mismatches 16;	Indels 5;	Gaps 4;

Oy	1933	ttgattcttcagacaggttaagtgaatctcaacaaagaagctgaactgctgt	1992
Db	743	ttgcgatttttcagacagatgatgtg- -ttccatgcagacagaaagtcgaatctgwc- t	687
Oy	1993	tttcacgaagaaggtctcagaagaagaagcctcttaattacttactgaactgct	2052
Db	686	tttccgagaaagagatctcaagaaagcagaccttccatttacttactgaactgct	627
Oy	2053	ctgataacataaacaagtcaagaagaacccactactgcttcsagaagagctcatccat	2112
Db	626	ctgatatatcaattagacattctcaagaagacacctatg- tcaagtcaaagctccatttccat	568
Oy	2113	aacccctctcgagagaccacaaatgaatgaactcaagaatagaatgatttaactctgct	2172
Db	567	actccctctcgagagaccacaaatgaatgaacttcaagatatgaatgatttaccttctgct	508
Oy	2173	aaatactatcgaagaagcgaagaataataataatagaacgaatagaagaagaatctcgaaacca	2232
Db	507	aaatatctatcgaagaagcgaagaataataataatagaacgaatagaagaagaatctcgaaaccg	448
Oy	2233	aatgcttgatattgaataaagaactgaattatttacaacaagaagaacagaaatttgaagt	2292
Db	447	aatgcgcgaatttgatataaagaaactgaattatttacaacaagaagaagaacaaatattgtact	388
Oy	2293	tcaacggtacagcttcttacaagactggttcgaagatagaagaagaatcagaatttttg	2352
Db	387	tcaccggtacagctcttttactgaactgttttcgaagactgaatgaagaagaatcagaatttttg	328
Oy	2353	ggtttcaacaactcacaagaagaagctgatacaag- tttagatattctggaga	2411
Db	327	gggtttcacaaactcacaagaagaagctgatacaagatggttttataatttttgggaaca	268
Oy	2412	ggaaatctcagatatctgttacaagcgltttcttcgctcccttcaactctacaattac	2471
Db	267	ggaaatctcagatatctgttacaagcggtttttctgcgtcccttcaactctacaatttacc	208
Oy	2472	tggcctttagaatattaaaaatgcatactcttcagaagtgaataagaatcatctctga	2531
Db	207	tggccttttgaattttttaaataatgcatactttttcaaaatgataaggaatcatctctga	148
Oy	2532	attttataaataatgataatgaaatctctagaattttttaccagcttgcgttcaagacc	2591
Db	147	atttttttataaataatgataatgaaatctttagaatttttttttaccagcttgcgttcaagacc	88
Oy	2592	aaatgaaataataaaaaaataatatttgaaatttctacagaattgataacctgataag	2651
Db	87	aaatgaaataatattttaaataataaatttttgcgattttttacagaattgataacctgataag	28
Oy	2652	aaaaaatcagaataca 2668	
Db	27	aaaaatttcagaaaaaa 11	

Search completed: December 27, 2001, 18:11:44
Job time: 4699 sec